

## A mixed relaxed clock model. Supplementary material

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**Running head:** Mixed clock

**Keywords:** Molecular dating, Relaxed molecular clock, Bayesian inference, Monte Carlo.

## Supplementary Tables

Table S1: Simulation results under the node-dating settings: true versus inferred proportion of variance contributed by the whitenoise component. Each pair of entries corresponds to a replicate simulated with parameter configurations drawn from the posterior distribution under the model indicated on the top line.

BROWNIAN		WHITENOISE		MIXED	
true	inferred	true	inferred	true	inferred
0%	3%	100%	97%	31%	26%
0%	4%	100%	99%	19%	28%
0%	2%	100%	98%	31%	27%
0%	3%	100%	96%	27%	24%
0%	2%	100%	97%	35%	37%
0%	2%	100%	99%	30%	38%
0%	2%	100%	99%	34%	16%
0%	2%	100%	99%	31%	53%
0%	2%	100%	99%	41%	30%
0%	2%	100%	99%	24%	15%

Table S2: Simulation results under the tip-dating settings: true versus inferred proportion of variance contributed by the whitenoise component. Each pair of entries corresponds to a replicate simulated with parameter configurations drawn from the posterior distribution under the model indicated on the top line, except for divergence times, which were drawn from the serial birth-death prior with diversified sampling.

BROWNIAN		WHITENOISE		MIXED	
true	inferred	true	inferred	true	inferred
0%	3%	100%	99%	47%	40%
0%	3%	100%	99%	40%	31%
0%	4%	100%	99%	38%	71%
0%	2%	100%	99%	42%	64%
0%	3%	100%	98%	37%	60%
0%	3%	100%	99%	50%	60%
0%	5%	100%	99%	45%	55%
0%	5%	100%	98%	47%	38%
0%	12%	100%	99%	36%	43%
0%	8%	100%	99%	35%	52%

Table S3: Simulation results under the tip-dating settings: true versus inferred proportion of variance contributed by the whitenoise component. Each pair of entries corresponds to a replicate simulated with parameter configurations drawn from the posterior distribution under the model indicated on the top line, except for divergence times, which were drawn from a serial Yule prior without diversified sampling.

BROWNIAN		WHITENOISE		MIXED	
true	inferred	true	inferred	true	inferred
0%	13%	100%	99%	47%	85%
0%	13%	100%	99%	40%	98%
0%	58%	100%	99%	38%	87%
0%	27%	100%	99%	42%	71%
0%	20%	100%	99%	37%	90%
0%	13%	100%	99%	50%	68%
0%	41%	100%	99%	45%	78%
0%	17%	100%	99%	47%	38%
0%	14%	100%	99%	36%	65%
0%	20%	100%	98%	35%	81%

Table S4: Simulation results under the tip-dating settings: true versus inferred proportion of variance contributed by the whitenoise component. Each pair of entries corresponds to a replicate simulated with parameter configurations drawn from the posterior distribution under the model indicated on the top line.

BROWNIAN		WHITENOISE		MIXED	
true	inferred	true	inferred	true	inferred
0%	11%	100%	97%	47%	19%
0%	45%	100%	99%	40%	60%
0%	14%	100%	92%	38%	28%
0%	9%	100%	99%	42%	49%
0%	18%	100%	99%	37%	48%
0%	18%	100%	99%	50%	45%
0%	16%	100%	95%	45%	65%
0%	25%	100%	99%	47%	44%
0%	14%	100%	99%	36%	26%
0%	28%	100%	98%	35%	34%

Table S5: Clade constraints used for estimating the tree topology for the tip-dating analysis.

<i>Metacheiromys marshi</i>	stem Pangolin
<i>Moeritherium lyonsi</i>	stem Elephant
<i>Notharctus tenebrosus</i>	Primates (stem or crown)
<i>Dawsonolagus antiquus</i>	stem Lagomorpha (1)
<i>Gomphos elkema</i>	stem Lagomorpha (2, i.e. older than <i>Dawsonolagus</i> )
<i>Paramys delicatus</i>	stem Rodentia
<i>Cocomys lingchaensis</i>	stem Rodentia
<i>Tribosphenomys minutus</i>	stem Rodentia
<i>Rhombomylus turpanensis</i>	stem Glires or Lagomorpha or Rodentia
<i>Didolodus multicuspis</i>	stem Cetartiodactyla + Perissodactyla
<i>Thomashuxleya externa</i>	stem Cetartiodactyla + Perissodactyla
<i>Protolipterna ellipsodontoides</i>	stem Cetartiodactyla + Perissodactyla
<i>Carodnia vieirai</i>	stem Cetartiodactyla + Perissodactyla

Table S5 (continued): Clade constraints used for estimating the tree topology for the tip-dating analysis.

<i>Vulpavus ovatus</i>	stem Carnivora
<i>Vulpavus profectus</i>	stem Carnivora
<i>Sinopa rapax</i>	stem Carnivora
<i>Meshippus bairdi</i>	stem Equidae
<i>Basilosaurus cetoides</i>	stem Cetacea (1)
<i>Artiocetus clavis</i>	stem Cetacea (2, i.e. older than <i>Basilosaurus</i> )
<i>Rodhocetus balochistanensis</i>	stem cetacea (3, i.e. older than <i>Artiocetus</i> )
<i>Archaeotherium mortoni</i>	stem Whippomorpha
<i>Icaronycteris index</i>	Chiroptera (stem or crown)
<i>Onychonycteris finneyi</i>	Chiroptera (stem or crown)
<i>Hyopsodus paulus</i>	Laurasiatheria (stem or crown)
<i>Apheliscus insidiosus</i>	Laurasiatheria (stem or crown)
<i>Phenacodus intermedius</i>	Laurasiatheria (stem or crown)
<i>Mesonyx obtusidens</i>	Laurasiatheria (stem or crown)
<i>Protungulatum donnae</i>	Laurasiatheria (stem or crown)
<i>Leptictis dakotensis</i>	stem Eutheria (1)
<i>Ukhaatherium nessovi</i>	stem Eutheria (2)
<i>Zalambdalestes lechei</i>	stem Eutheria (2)
<i>Maelestes gobiensis</i>	stem Eutheria (2)
<i>Eomaia scansoria</i>	stem Eutheria (3)

Table S6: Fossil calibrations (My) used for the node-dating analysis. For each calibration, the calibrated node is referred to by two species, of which the node is the last common ancestor.

<b>Species 1</b>	<b>Species 2</b>	<b>Upper calibration</b>	<b>Lower calibration</b>
Cyclopes didactylus	Tamandua tetradactyla	61.1	15.97
Bradypus tridactylus	Choloepus sp.	40.6	15.97
Cyclopes didactylus	Choloepus sp.	65.5	31.5
Cyclopes didactylus	Dasybus novemcinctus	71.2	58.5
Dugong dugon	Trichechus manatus	40.6	31.4
Elephantulus rufescens	Rhynchocyon cirnei	56	15.97
Dugong dugon	Procavia capensis	71.2	55.6
Ochotona sp.	Oryctolagus cuniculus	61.1	48.4
Nycteris thebaica	Saccopteryx bilineata	58.9	40.2
Hipposideros commersoni	Rhinolophus creaghi	56	37.1
Megaderma lyra	Craseonycteris thonglongyai	48.8	33.8
Myotis lucifugus	Tadarida brasiliensis	56	37.1
Myotis lucifugus	Natalus stramineus	61.1	48.4
Pteronotus parnellii	Artibeus jamaicensis	40.6	28.3
Furipterus horrens	Noctilio sp.	34	5.332
Hipposideros commersoni	Myotis lucifugus	61.1	48.4
Canis lupus familiaris	Phoca vitulina	56	37.1
Ailuropoda melanoleuca	Phoca vitulina	48.8	33.8
Mephitis mephitis	Phoca vitulina	48.8	33.8
Procyon lotor	Meles meles	40.6	27.6
Procyon lotor	Mephitis mephitis	40.6	30.9
Felis silvestris	Prionodon linsang	40.6	28.3
Suricata suricatta	Canis lupus familiaris	65.8	37.1

Table S6 (continued): Fossil calibrations (My) used for the node-dating analysis. For each calibration, the calibrated node is referred to by two species, of which the node is the last common ancestor.

<b>Species 1</b>	<b>Species 2</b>	<b>Upper calibration</b>	<b>Lower calibration</b>
<i>Nycticebus coucang</i>	<i>Otolemur garnettii</i>	56	37.1
<i>Tarsius syrichta</i>	<i>Homo sapiens</i>	58.9	37.1
<i>Homo sapiens</i>	<i>Saimiri sciureus</i>	56	28.3
<i>Lemur catta catta</i>	<i>Otolemur garnettii</i>	56	37.1
<i>Tupaia glis</i>	<i>Ptilocercus lowii</i>	65.8	37.1
<i>Equus caballus</i>	<i>Tapirus indicus</i>	61.1	55.5
<i>Erinaceus europaeus</i>	<i>Sorex araneus</i>	84.2	61.1
<i>Erinaceus europaeus</i>	<i>Podogymnura truei</i>	48.8	28.3
<i>Lama glama</i>	<i>Tragulus napu</i>	65.8	52.5
<i>Sus scrofa</i>	<i>Pecari tajacu</i>	37.3	15.97
<i>Hippopotamus amphibius</i>	<i>Tursiops truncatus</i>	61.1	52.5
<i>Tursiops truncatus</i>	<i>Caperea marginata</i>	48.8	33.8
<i>Ictidomys tridecemlineatus</i>	<i>Aplodontia rufa</i>	58.9	45.7
<i>Ictidomys tridecemlineatus</i>	Gliridae	61.1	48.4
<i>Dinomys branickii</i>	<i>Chinchilla lanigera</i>	37.3	24.5
<i>Cavia porcellus</i>	<i>Dasyprocta punctata</i>	37.3	24.5
<i>Anomalurus beecrofti</i>	<i>Pedetes</i> sp.	56	37.1
<i>Hystrix</i> sp.	<i>Cavia porcellus</i>	56	33.8
Geomyidae	<i>Dipodomys heermanni</i>	40.6	31.4
<i>Dipodomys heermanni</i>	<i>Castor canadensis</i>	61.1	52.4
<i>Spalax</i> sp.	<i>Jaculus jaculus</i>	58.9	45
<i>Laonastes aenigmamus</i>	<i>Ctenodactylus gundi</i>	48.8	28.3
<i>Ictidomys tridecemlineatus</i>	<i>Hystrix</i> sp.	65.8	55.6
<i>Pedetes</i> sp.	<i>Castor canadensis</i>	65.8	52.4

Table S7: Fossil age constraints (My) used for the tip-dating analysis.

<b>Species</b>	<b>Upper calibration</b>	<b>Lower calibration</b>
<i>Eomaia scansoria</i>	124.4	122.2
<i>Maelestes gobiensis</i>	83.6	72.1
<i>Metacheiromys marshi</i>	50.3	46.2
<i>Ukhaatherium nessovi</i>	83.6	72.1
<i>Zalambdalestes lechei</i>	83.6	72.1
<i>Leptictis dakotensis</i>	37.2	33.3
<i>Moeritherium lyonsi</i>	37.2	33.9
<i>Notharctus tenebrosus</i>	50.3	46.2
<i>Protungulatum donnae</i>	66.0	63.3
<i>Apheliscus insidiosus</i>	55.8	50.3
<i>Phenacodus intermedius</i>	56.8	55.8
<i>Protolipterna ellipsodontoides</i>	59.0	57.5
<i>Hyopsodus paulus</i>	50.3	46.2
<i>Didolodus multicuspis</i>	54.0	51.0
<i>Carodnia vieirai</i>	59.0	57.5
<i>Thomashuxleya externa</i>	54.0	51.0

Table S7 (continued): Fossil age constraints (My) used for the tip-dating analysis.

<b>Species</b>	<b>Upper calibration</b>	<b>Lower calibration</b>
Vulpavus ovatus	50.3	46.2
Vulpavus profectus	50.4	46.2
Sinopa rapax	50.5	46.2
Dawsonolagus antiquus	54	53
Gomphos elkema	56	55
Rhombomylus turpanensis	54	53
Tribosphenomys minutus	59	57
Paramys delicatus	55.4	50.3
Cocomys lingchaensis	56	55
Meshippus bairdi	38.0	33.9
Basilosaurus cetoides	40.4	37.2
Mesonyx obtusidens	50.3	46.2
Archaeotherium mortoni	38.0	33.9
Artiocetus clavis	48.4	46
Rodhocetus balochistanensis	48.4	46
Icaronycteris index	52.5	50.3
Onychonycteris finneyi	52.5	50.3

# Supplementary Figures

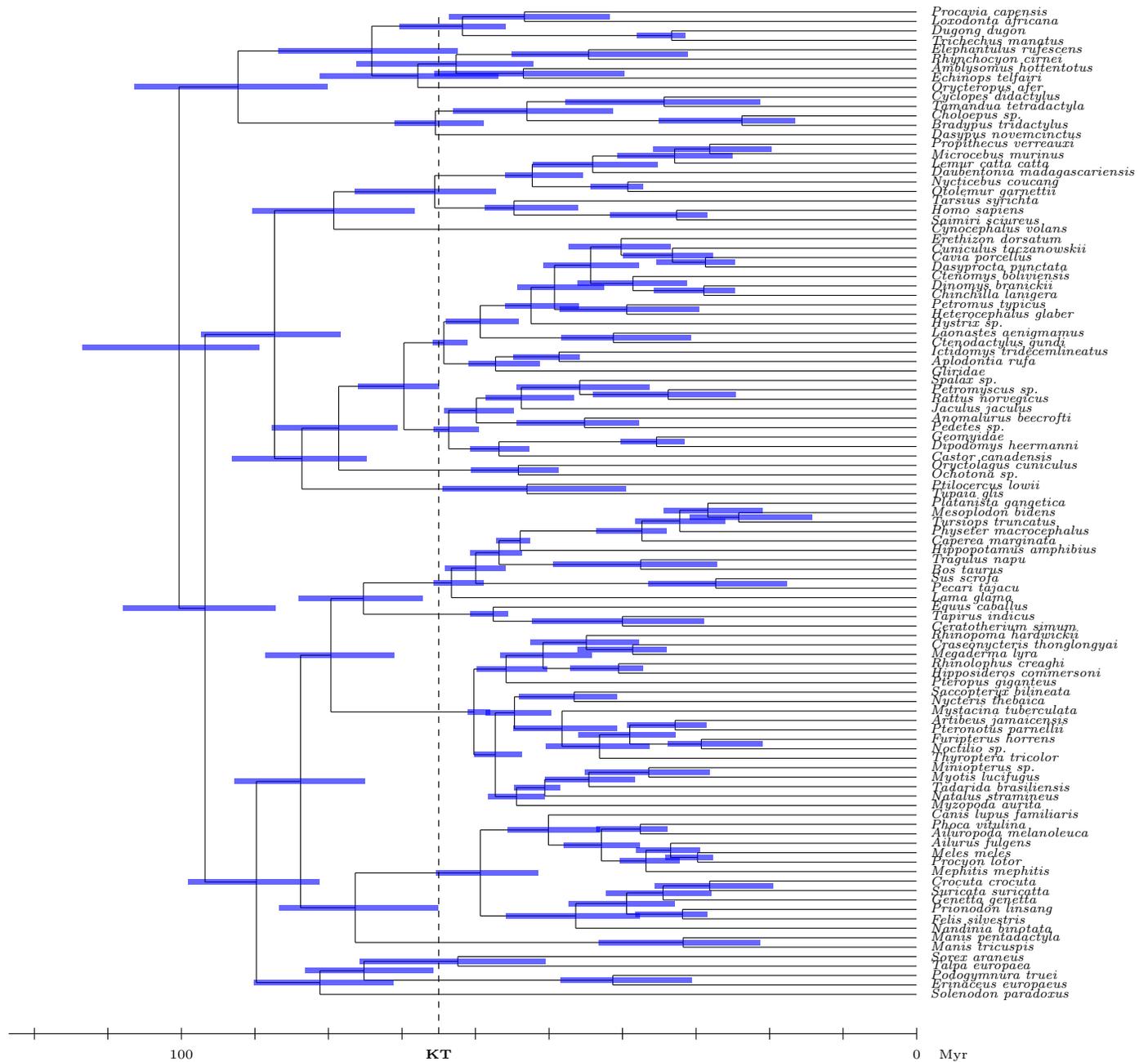


Figure S1. Inferred divergence times (posterior median, blue bars: 95% credible intervals) under the whitenoise clock, using the node-dating approach.

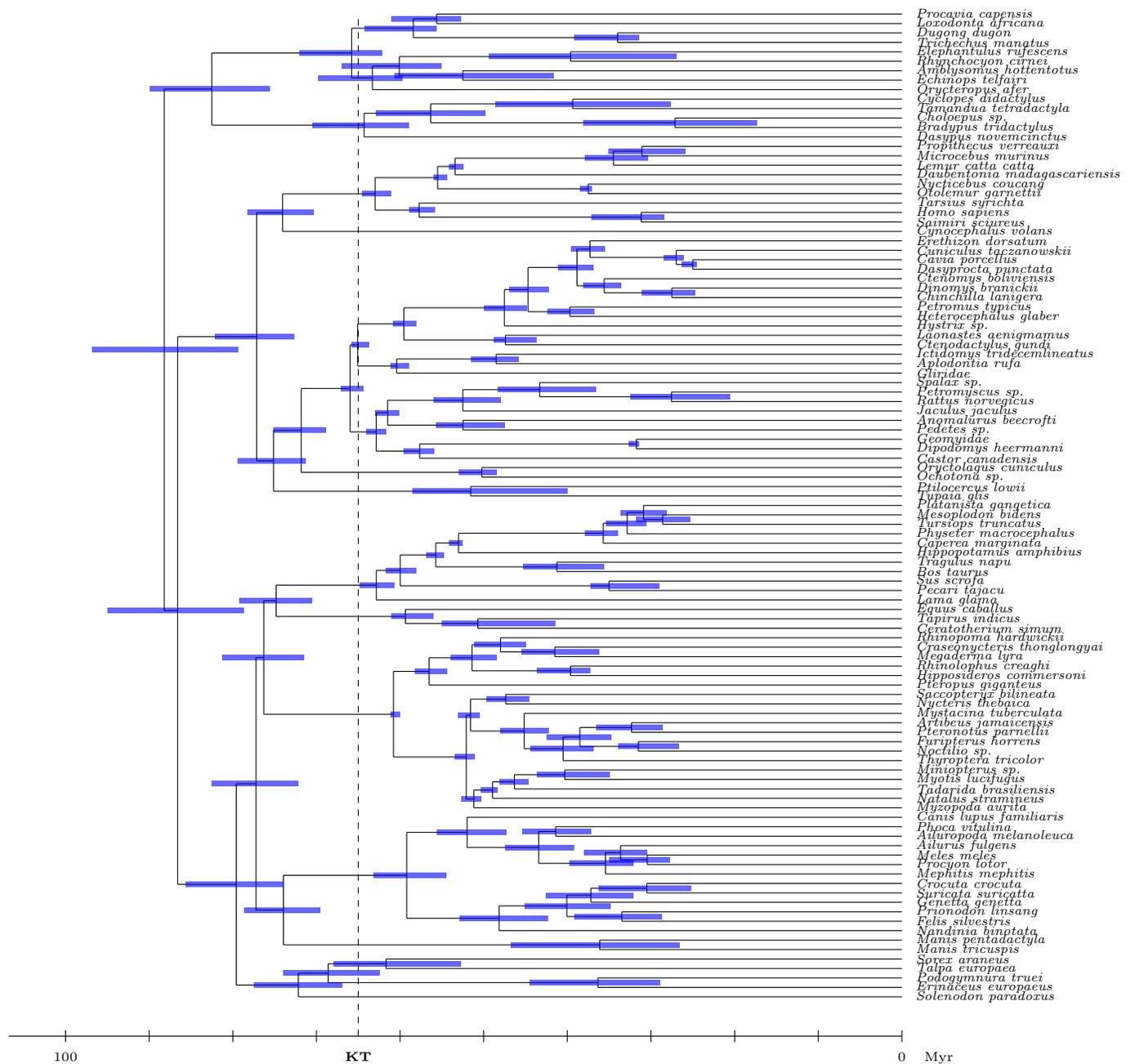


Figure S2. Inferred divergence times (posterior median, blue bars: 95% credible intervals) under the Brownian clock, using the node-dating approach.

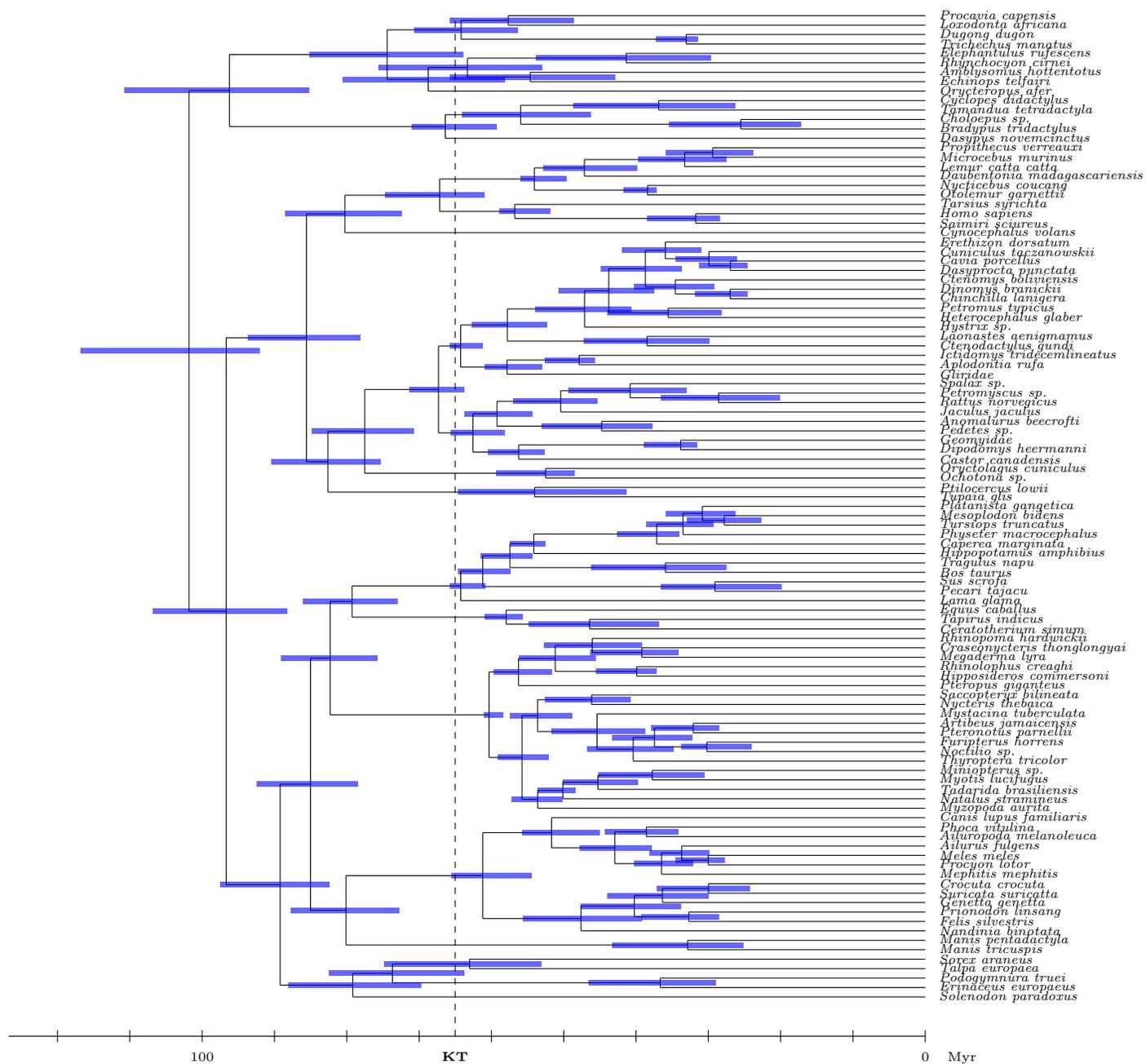


Figure S3. Inferred divergence times (posterior median, blue bars: 95% credible intervals) under the mixed clock, using the node-dating approach.

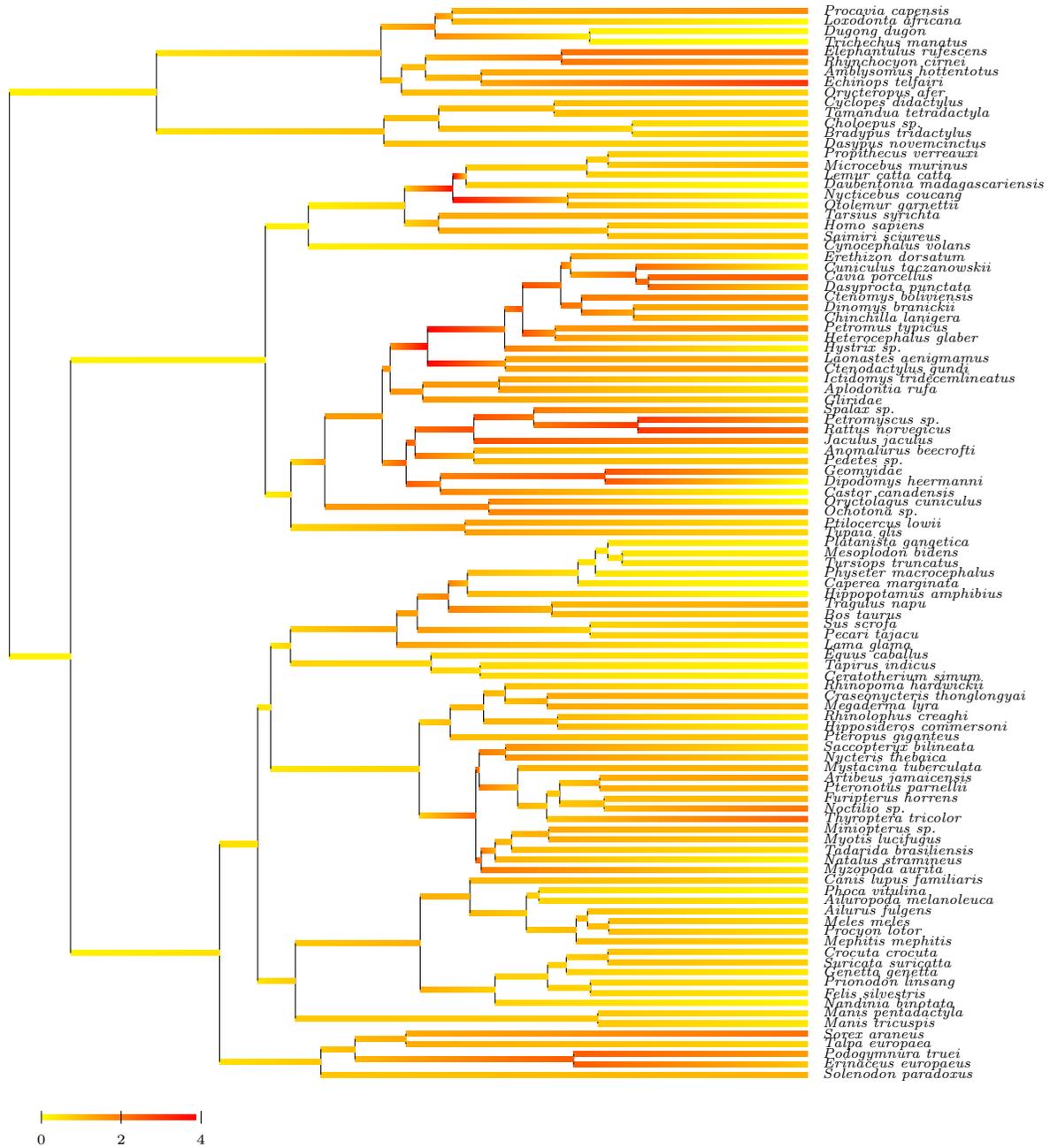


Figure S4. Inferred history of rate variation under the Brownian clock, using the node-dating approach.

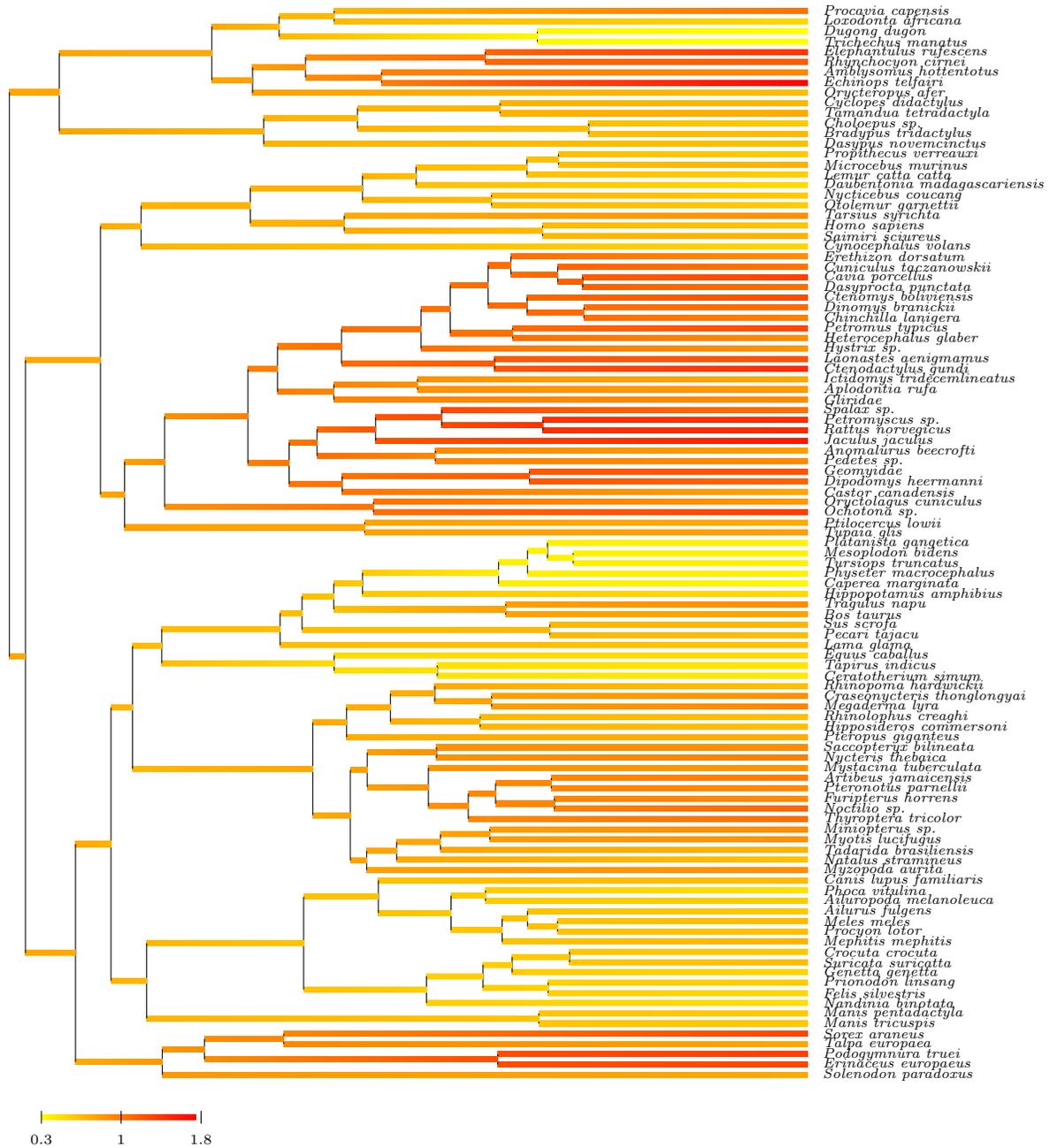


Figure S5. Inferred history of long-term rate variation (Brownian component of the mixed clock) using the node-dating approach.

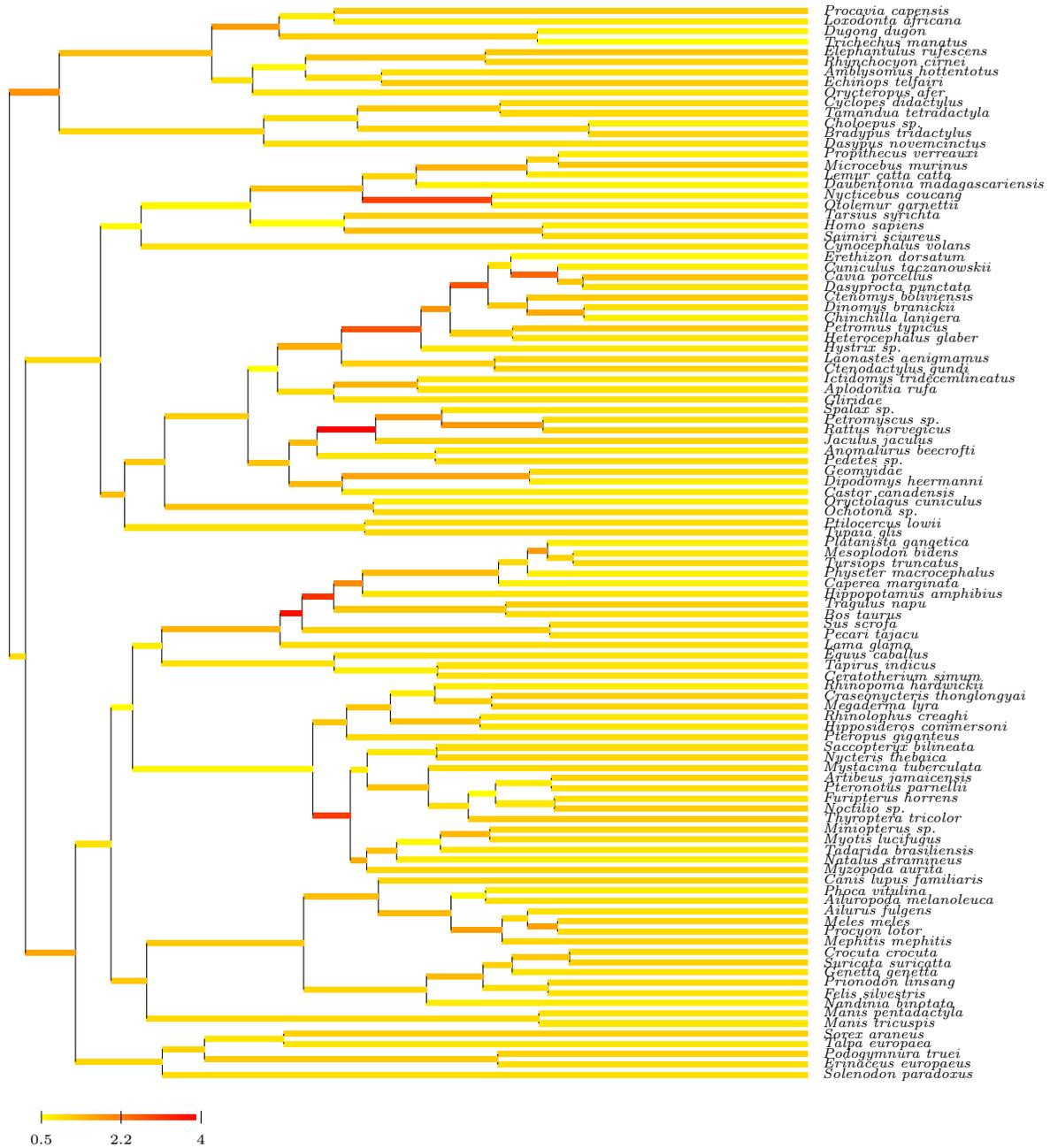


Figure S6. Inferred history of short-term rate variation (whitenoise component of the mixed clock) using the node-dating approach.







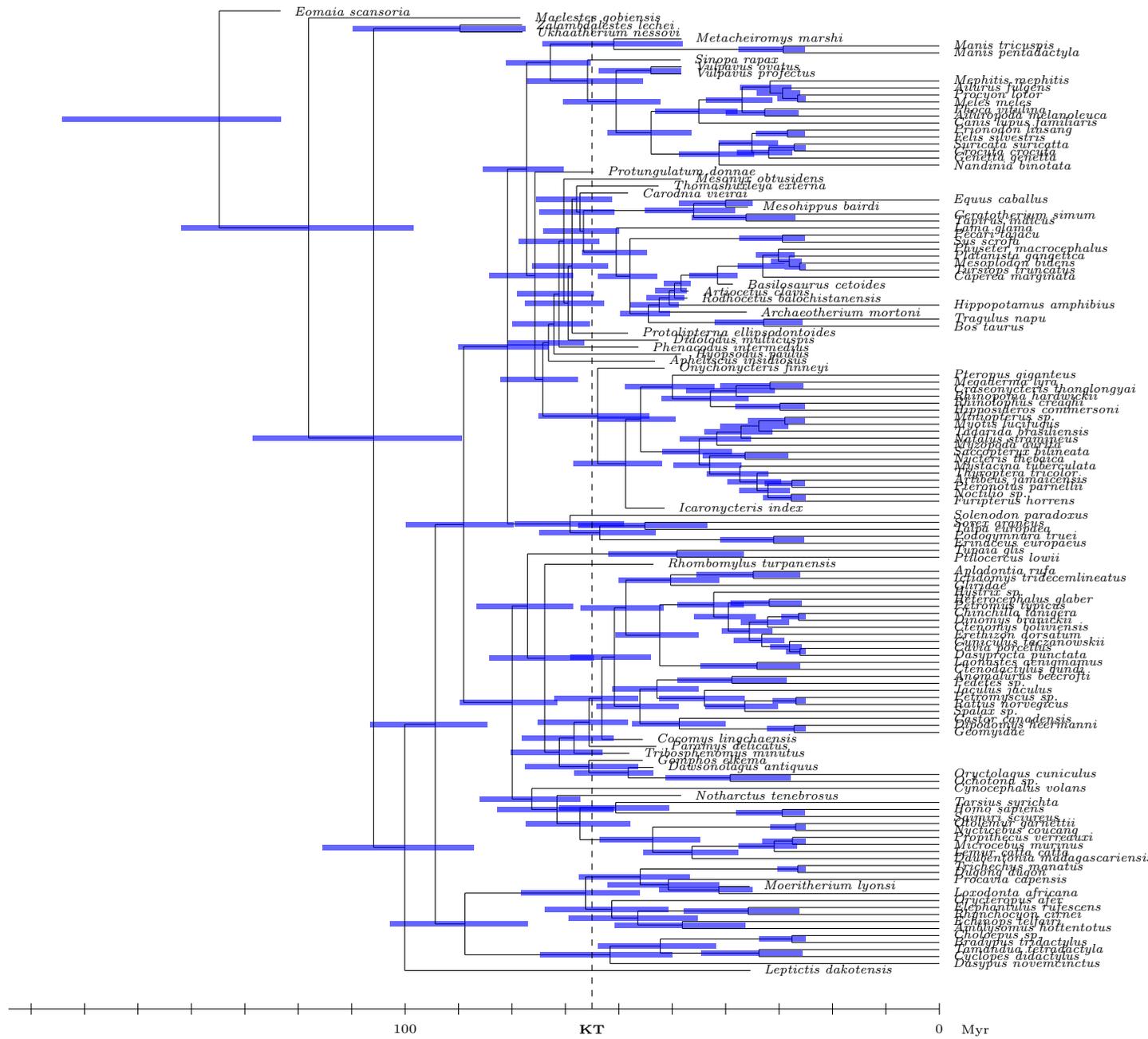


Figure S10. Inferred divergence times (posterior median, blue bars: 95% credible intervals) under the mixed clock, using the tip-dating approach and with morphological characters.